

THE INFLUENCE OF SULFATE ON METHANOGENIC LCFA-DEGRADING MICROBIAL COMMUNITIES

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ABSTRACT

Long chain fatty-acids (LCFA) are the main product of lipids hydrolysis, and are commonly found in several types of wastewaters. Through effective anaerobic treatment, LCFA can be microbiologically converted to large amounts of biogas, a renewable source of energy. However, in wastewaters containing sulfate, the potential for the energetic valorization of LCFA through production of methane-rich biogas can decrease due to a total or partial inhibition of methanogenesis. In this way, it is crucial to get more insight on the potential competition of syntrophs and methanogens with sulfate-reducing bacteria (SRB) during LCFA degradation. By inferring microbial population dynamics in LCFA-degrading sludges submitted to contact with sulfate one might address basic questions that might be important in the anaerobic digestion process control.

In this work, a combined approach of molecular microbial ecology techniques and cultivation experiments was used to study the effect of sulfate on microbial LCFA-degrading methanogenic communities. Bacterial community dynamics in distinct enrichment series, growing on oleate (unsaturated, C18:1) or palmitate (saturated, C16:0), and submitted to incubations with 10 mM sulfate, were studied by 16S rRNA gene denaturing gradient gel electrophoresis (DGGE)-fingerprinting analysis and subsequent sequence analysis. Phylogenetic affiliation of rRNA gene sequences corresponding to predominant DGGE-bands demonstrated that members of the *Syntrophomonadaceae* and *Syntrophobacteraceae* families, together with sulfate-reducers mainly belonging to the *Desulfovibrionales* order, were present in the sulfate-reducing enrichment cultures. Competition between SRB and methanogens in these enrichment cultures was surveyed by relative quantification of archaea, using real-time PCR. Addition of sulfate to methanogenic cultures resulted in the inhibition of methanogenesis, and archaea could no longer be detected by real-time PCR. Competition for hydrogen and acetate was therefore won by sulfate-reducers, but acetogenic bacteria were still the LCFA-degrading organisms present after subculturing with sulfate. In this way, methanogenesis was directly affected by the presence of sulfate in the medium, indicating that even low concentrations of sulfate may impair the efficient conversion of LCFA to methane.